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OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,119

DATE: 04/19/2001

TIME: 12:05:04

Input Set : A:\es.txt

Output Set: N:\CRF3\04192001\I823119.raw

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5 <110> APPLICANT: Kaplow, June  
 7 Haws, Thomas  
 9 Rosier, Marie  
 11 Denefle, Patrice  
 15 <120> TITLE OF INVENTION: NUCLEAR FACTOR KB INDUCING FACTOR  
 19 <130> FILE REFERENCE: 23461 usa  
 C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/823,119  
 C--> 25 <141> CURRENT FILING DATE: 2001-03-30  
 29 <160> NUMBER OF SEQ ID NOS: 5  
 33 <170> SOFTWARE: PatentIn Ver. 2.0  
 37 <210> SEQ ID NO: 1  
 39 <211> LENGTH: 453  
 41 <212> TYPE: PRT  
 43 <213> ORGANISM: Homo sapiens  
 48 <400> SEQUENCE: 1  
 50 Met Ala Leu Val Arg Ala Leu Val Cys Cys Leu Leu Thr Ala Trp His  
 52 1 5 10 15  
 56 Cys Arg Ser Gly Leu Gly Leu Pro Val Ala Pro Ala Gly Gly Arg Asn  
 58 20 25 30  
 62 Pro Pro Pro Ala Ile Gly Gln Phe Trp His Val Thr Asp Leu His Leu  
 64 35 40 45  
 68 Asp Pro Thr Tyr His Ile Thr Asp Asp His Thr Lys Val Cys Ala Ser  
 70 50 55 60  
 74 Ser Lys Gly Ala Asn Ala Ser Asn Pro Gly Pro Phe Gly Asp Val Leu  
 76 65 70 75 80  
 80 Cys Asp Ser Pro Tyr Gln Leu Ile Leu Ser Ala Phe Asp Phe Ile Lys  
 82 85 90 95  
 86 Asn Ser Gly Gln Glu Ala Ser Phe Met Ile Trp Thr Gly Asp Ser Pro  
 88 100 105 110  
 92 Pro His Val Pro Val Pro Glu Leu Ser Thr Asp Thr Val Ile Asn Val  
 94 115 120 125  
 98 Ile Thr Asn Met Thr Thr Thr Ile Gln Ser Leu Phe Pro Asn Leu Gln  
 100 130 135 140  
 104 Val Phe Pro Ala Leu Gly Asn His Asp Tyr Trp Pro Gln Asp Gln Leu  
 106 145 150 155 160  
 110 Ser Val Val Thr Ser Lys Val Tyr Asn Ala Val Ala Asn Leu Trp Lys  
 112 165 170 175  
 116 Pro Trp Leu Asp Glu Glu Ala Ile Ser Thr Leu Arg Lys Gly Gly Phe  
 118 180 185 190  
 122 Tyr Ser Gln Lys Val Thr Thr Asn Pro Asn Leu Arg Ile Ile Ser Leu  
 124 195 200 205  
 128 Asn Thr Asn Leu Tyr Tyr Gly Pro Asn Ile Met Thr Leu Asn Lys Thr  
 130 210 215 220  
 134 Asp Pro Ala Asn Gln Phe Glu Trp Leu Glu Ser Thr Leu Asn Asn Ser  
 136 225 230 235 240  
 140 Gln Gln Asn Lys Glu Lys Val Tyr Ile Ile Ala His Val Pro Val Gly  
 142 245 250 255

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146 Tyr Leu Pro Ser Ser Gln Asn Ile Thr Ala Met Arg Glu Tyr Tyr Asn
148      260      265      270
152 Glu Lys Leu Ile Asp Ile Phe Gln Lys Tyr Ser Asp Val Ile Ala Gly
154      275      280      285
158 Gln Phe Tyr Gly His Thr His Arg Asp Ser Ile Met Val Leu Ser Asp
160      290      295      300
164 Lys Lys Gly Ser Pro Val Asn Ser Leu Phe Val Ala Pro Ala Val Thr
166 305      310      315      320
170 Pro Val Lys Ser Val Leu Glu Lys Gln Thr Asn Asn Pro Gly Ile Arg
172      325      330      335
176 Leu Phe Gln Tyr Asp Pro Arg Asp Tyr Lys Leu Leu Asp Met Leu Gln
178      340      345      350
182 Tyr Tyr Leu Asn Leu Thr Glu Ala Asn Leu Lys Gly Glu Ser Ile Trp
184      355      360      365
188 Lys Leu Glu Tyr Ile Leu Thr Gln Thr Tyr Asp Ile Glu Asp Leu Gln
190      370      375      380
194 Pro Glu Ser Leu Tyr Gly Leu Ala Lys Gln Phe Thr Ile Leu Asp Ser
196 385      390      395      400
200 Lys Gln Phe Ile Lys Tyr Tyr Asn Tyr Phe Phe Val Ser Tyr Asp Ser
202      405      410      415
206 Ser Val Thr Cys Asp Lys Thr Cys Lys Ala Phe Gln Ile Cys Ala Ile
208      420      425      430
212 Met Asn Leu Asp Asn Ile Ser Tyr Ala Asp Cys Leu Lys Gln Leu Tyr
214      435      440      445
218 Ile Lys His Asn Tyr
220      450
226 <210> SEQ ID NO: 2
228 <211> LENGTH: 364
230 <212> TYPE: PRT
232 <213> ORGANISM: Homo sapiens
236 <400> SEQUENCE: 2
238 Met Ala Leu Val Arg Ala Leu Val Cys Cys Leu Leu Thr Ala Trp His
240 1      5      10      15
244 Cys Arg Ser Gly Leu Gly Leu Pro Val Ala Pro Ala Gly Gly Arg Asn
246      20      25      30
250 Pro Pro Pro Ala Ile Gly Gln Phe Trp His Val Thr Asp Leu His Leu
252      35      40      45
256 Asp Pro Thr Tyr His Ile Thr Asp Asp His Thr Lys Val Cys Ala Ser
258      50      55      60
262 Ser Lys Gly Ala Asn Ala Ser Asn Pro Gly Pro Phe Gly Asp Val Leu
264 65      70      75      80
268 Cys Asp Ser Pro Tyr Gln Leu Ile Leu Ser Ala Phe Asp Phe Ile Lys
270      85      90      95
274 Asn Ser Gly Gln Glu Ala Ser Phe Met Ile Trp Thr Gly Asp Ser Pro
276      100      105      110
280 Pro His Val Pro Val Pro Glu Leu Ser Thr Asp Thr Val Ile Asn Val
282      115      120      125
286 Ile Thr Asn Met Thr Thr Thr Ile Gln Ser Leu Phe Pro Asn Leu Gln
288      130      135      140

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292 Val Phe Pro Ala Leu Gly Asn His Asp Tyr Trp Pro Gln Val Tyr Ile
294 145                               150                               155                               160
298 Ile Ala His Val Pro Val Gly Tyr Leu Pro Ser Ser Gln Asn Ile Thr
300                               165                               170                               175
304 Ala Met Arg Glu Tyr Tyr Asn Glu Lys Leu Ile Asp Ile Phe Gln Lys
306                               180                               185                               190
310 Tyr Ser Asp Val Ile Ala Gly Gln Phe Tyr Gly His Thr His Arg Asp
312                               195                               200                               205
316 Ser Ile Met Val Leu Ser Asp Lys Lys Gly Ser Pro Val Asn Ser Leu
318                               210                               215                               220
322 Phe Val Ala Pro Ala Val Thr Pro Val Lys Ser Val Leu Glu Lys Gln
324 225                               230                               235                               240
328 Thr Asn Asn Pro Gly Ile Arg Leu Phe Gln Tyr Asp Pro Arg Asp Tyr
330                               245                               250                               255
334 Lys Leu Leu Asp Met Leu Gln Tyr Tyr Leu Asn Leu Thr Glu Ala Asn
336                               260                               265                               270
340 Leu Lys Gly Glu Ser Ile Trp Lys Leu Glu Tyr Ile Leu Thr Gln Thr
342                               275                               280                               285
346 Tyr Asp Ile Glu Asp Leu Gln Pro Glu Ser Leu Tyr Gly Leu Ala Lys
348                               290                               295                               300
352 Gln Phe Thr Ile Leu Asp Ser Lys Gln Phe Ile Lys Tyr Tyr Asn Tyr
354 305                               310                               315                               320
358 Phe Phe Val Ser Tyr Asp Ser Ser Val Thr Cys Asp Lys Thr Cys Lys
360                               325                               330                               335
364 Ala Phe Gln Ile Cys Ala Ile Met Asn Leu Asp Asn Ile Ser Tyr Ala
366                               340                               345                               350
370 Asp Cys Leu Lys Gln Leu Tyr Ile Lys His Asn Tyr
372                               355                               360

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378 &lt;210&gt; SEQ ID NO: 3

380 &lt;211&gt; LENGTH: 1362

382 &lt;212&gt; TYPE: DNA

384 &lt;213&gt; ORGANISM: Homo sapiens

388 &lt;400&gt; SEQUENCE: 3

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390 atggcgctgg tgcgcgcact cgtctgctgc ctgctgactg cctggcactg ccgctccggc 60
392 ctcgggctgc ccgtggcgcc cgcaggcggc aggaatcctc ctccggcgat aggacagttt 120
394 tggcatgtga ctgacttaca cttagaccct acttaccaca tcacagatga ccacacaaaa 180
396 gtgtgtgctt catctaaagg tgcaaatgcc tccaaccctg gcccttttgg agatgttctg 240
398 tgtgattctc catatcaact tattttgtca gcatttgatt ttattaaaaa ttctggacaa 300
400 gaagcatctt tcatgatatg gacaggggat agcccacctc atgttctctg acctgaactc 360
402 tcaacagaca ctgttataaa tgtgatcact aatatgacaa ccaccatcca gagtctcttt 420
404 ccaaattctc aggttttccc tgcgctgggt aatcatgact attggccaca ggatcaactg 480
406 tctgtagtca ccagtaaagt gtacaatgca gtagcaaacc tctggaaacc atggctagat 540
408 gaagaagcta ttagtacttt aaggaaaagt ggtttttatt cacagaaagt tacaactaat 600
410 ccaaacctta ggatcatcag tctaaacaca aacttgtact acggcccaaa tataatgaca 660
412 ctgaacaaga ctgaccagc caaccagttt gaatggctag aaagtacatt gaacaactct 720
414 cagcagaata aggagaaggt gtatatcata gcacatgttc cagtggggtg tctgccatct 780
416 tcacagaaca tcacagcaat gagagaatac tataatgaga aattgataga tatttttcaa 840
418 aaatacagtg atgtcattgc aggacaattt tatggacaca ctacagaga cagcattatg 900
420 gttcttttcg ataaaaaagg aagtccagta aattctttgt ttgtggctcc tgctgttaca 960

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422 ccagtgaaga gtgtttttaga aaaacagacc aacaatcctg gtatcagact gtttcagtat 1020
424 gatcctcgtg attataaaatt attggatatg ttgcagtatt acttgaatct gacagagggc 1080
426 aatctaaagg gagagtccat ctggaagctg gagtatatcc tgacccagac ctacgacatt 1140
428 gaagatttgc agccggaaaag tttatatgga ttagctaaac aattttacaat cctagacagt 1200
430 aagcagttta taaaatacta caattacttc tttgtgagtt atgacagcag tgtaacatgt 1260
432 gataagacat gtaaggcctt tcagatttgt gcaattatga atcttgataa tatttcctat 1320
434 gcagattgcc tcaaacagct ttatataaag cacaattact ag 1362

```

438 &lt;210&gt; SEQ ID NO: 4

440 &lt;211&gt; LENGTH: 1095

442 &lt;212&gt; TYPE: DNA

444 &lt;213&gt; ORGANISM: Homo sapiens

448 &lt;400&gt; SEQUENCE: 4

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450 atggcgctgg tgcgcgcact cgtctgctgc ctgctgactg cctggcactg ccgctccggc 60
452 ctcgggctgc ccgtggcgcc cgcaggcgcc aggaatcctc ctccggcgat aggacagttt 120
454 tggcatgtga ctgacttaca cttagaccct acttaccaca tcacagatga ccacacaaaa 180
456 gtgtgtgctt catctaaagg tgcaaagtc tccaaccctg gcccttttgg agatgttctg 240
458 tgtgattctc catatcaact tattttgtca gcatttgatt ttattaaaaa ttctggacaa 300
460 gaagcatctt tcatgatatg gacaggggat agcccacctc atgttcctgt acctgaactc 360
462 tcaacagaca ctgttataaa tgtgatcact aatatgacaa ccaccatcca gagtctcttt 420
464 ccaaattctc aggttttccc tgcgctgggt aatcatgact attggccaca ggtgtatata 480
466 atagcacatg ttccagtggg gtatctgcc tcttcacaga acatcacagc aatgagagaa 540
468 tactataatg agaaattgat agatattttt caaaagtaca gtgatgtcat tgcaggacaa 600
470 ttttatggac aactcacag agacagcatt atggttcttt cagataaaaa aggaagtcca 660
472 gtaaattctt tgtttgtggc tctgctgtt acaccagtga agagtgtttt agaaaaacag 720
474 accaacaatc ctggtatcag actgtttcag tatgatcctc gtgattataa attattggat 780
476 atgttgagc attacttgaa tctgacagag gcgaatctaa agggagagtc catctggaag 840
478 ctggagtata tctgaccca gacctacgac attgaagatt tgcagccgga aagtttatat 900
480 ggattagcta aacaatttac aatcctagac agtaagcagt ttataaaata ctacaattac 960
482 ttctttgtga gttatgacag cagtgtaca tgtgataaga catgtaaggc ctttcagatt 1020
484 tgtgcaatta tgaatcttga taatatttcc tatgcagatt gcctcaaaca gctttatata 1080
486 aagcacaatt actag 1095

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490 &lt;210&gt; SEQ ID NO: 5

492 &lt;211&gt; LENGTH: 15

494 &lt;212&gt; TYPE: PRT

496 &lt;213&gt; ORGANISM: Homo sapiens

500 &lt;400&gt; SEQUENCE: 5

502 Ser Lys Gly Ala Asn Ala Ser Asn Pro Gly Pro Phe Gly Asp Val

504 1 5 10 15

VERIFICATION SUMMARY

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Input Set : A:\es.txt

Output Set: N:\CRF3\04192001\I823119.raw

L:23 M:270 C: Current Application Number differs, Replaced Current Application Number

L:25 M:271 C: Current Filing Date differs, Replaced Current Filing Date